



SEQUENCE LISTING

<110> Ullrich, Axel
Aoki, Naohito
Kim, Yeong Woong
Wang, Hong Yang
Chen, Zhengjun
Nayler, Oliver
Kharitonenkov, Alexei

<120> NOVEL PTP-20, PCP-2, BDP1, CLK, AND SIRP PROTEINS
AND RELATED PRODUCTS AND METHODS

<130> 034536-1481

<140> 10/087,993
<141> 2002-03-05

<150> 08/877,150
<151> 1997-06-17

<150> 60/023,485
<151> 1996-11-13

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<150> 60/030,964
<151> 1996-11-15

<150> 60/034,286
<151> 1996-12-19

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<170> PatentIn Ver. 3.2

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<222> (3)
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1 5

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<220>
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<223> Ser, Ile or Val

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<220>
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Arg Trp Xaa Met Xaa Trp
1 5

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 1 5 10 15

Trp Asp Tyr Gly Thr Trp Arg Ser Ser Ser His Lys Arg Lys Lys
 20 25 30

Arg Ser His Ser Ser Ala Arg Glu Gln Lys Arg Cys Arg Tyr Asp His
 35 40 45

Ser Lys Thr Thr Asp Ser Tyr Tyr Leu Glu Ser Arg Ser Ile Asn Glu
 50 55 60

Lys Ala Tyr His Ser Arg Arg Tyr Val Asp Glu Tyr Arg Asn Asp Tyr
 65 70 75 80

Met Gly Tyr Glu Pro Gly His Pro Tyr Gly Glu Pro Gly Ser Arg Tyr
 85 90 95

Gln Met His Ser Ser Lys Ser Ser Gly Arg Ser Gly Arg Ser Ser Tyr
 100 105 110

Lys Ser Lys His Arg Ser Arg His His Thr Ser Asp His His Ser His
 115 120 125

Gly His Ser His Arg Arg Lys Arg Ser Arg Ser Val Glu Asp Asp Glu
 130 135 140

Glu Gly His Leu Ile Cys Gln Ser Gly Asp Val Leu Ser Ala Arg Tyr
 145 150 155 160

Glu Ile Val Asp Thr Leu Gly Glu Gly Ala Phe Gly Lys Val Val Glu
 165 170 175

Cys Ile Asp His Lys Val Gly Gly Arg Arg Val Ala Val Lys Ile Val
 180 185 190

Lys Asn Val Asp Arg Tyr Cys Glu Ala Ala Gln Ser Glu Ile Gln Val
 195 200 205

Leu Glu His Leu Asn Thr Thr Asp Pro His Ser Thr Phe Arg Cys Val
 210 215 220

Gln Met Leu Glu Trp Phe Glu His Arg Gly His Ile Cys Ile Val Phe
 225 230 235 240

Glu Leu Leu Gly Leu Ser Thr Tyr Asp Phe Ile Lys Glu Asn Ser Phe
 245 250 255

Leu Pro Phe Arg Met Asp His Ile Arg Lys Met Ala Tyr Gln Ile Cys
 260 265 270

Lys Ser Val Asn Phe Leu His Ser Asn Lys Leu Thr His Thr Asp Leu
 275 280 285

Lys Pro Glu Asn Ile Leu Phe Val Lys Ser Asp Tyr Thr Glu Ala Asn
 290 295 300

Pro Lys Met Lys Arg Asp Glu Arg Thr Ile Val Asn Pro Asp Ile Lys
 305 310 315 320

Val Val Asp Phe Gly Ser Ala Thr Tyr Asp Asp Glu His His Ser Thr
 325 330 335

Leu Val Ser Thr Arg His Tyr Arg Ala Pro Glu Val Ile Leu Ala Leu
 340 345 350

Gly Trp Ser Gln Pro Cys Asp Val Trp Ser Ile Gly Cys Ile Leu Ile
 355 360 365

Glu Tyr Tyr Leu Gly Phe Thr Val Phe Pro Thr His Asp Ser Arg Glu
 370 375 380

His Leu Ala Met Met Glu Arg Ile Leu Gly Pro Leu Pro Lys His Met
 385 390 395 400

Ile Gln Lys Thr Arg Lys Arg Arg Tyr Phe His His Asp Arg Leu Asp
 405 410 415

Trp Asp Glu His Ser Ser Ala Gly Arg Tyr Val Ser Arg Arg Cys Lys
 420 425 430

Pro Leu Lys Glu Phe Met Leu Ser Gln Asp Ala Glu His Glu Phe Leu
 435 440 445

Phe Asp Leu Val Gly Lys Ile Leu Glu Tyr Asp Pro Ala Lys Arg Ile
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Thr Leu Lys Glu Ala Leu Lys His Pro Phe Phe Tyr Pro Leu Lys Lys
 465 470 475 480

His Thr

<210> 6
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 ctctgtgtcc acagcagtgc tggctgt

<210> 7
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<212> PRT
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 <220>
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 <400> 7
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 <222> (5)
 <223> Tyr or Phe

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 1 5

<210> 9
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28

<210> 10
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<210> 11
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<220>
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<400> 11
Asp Leu Lys Pro Glu Asn
1 5

<210> 12
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<210> 15
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<212> DNA
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36

<210> 21

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<212> DNA

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<400> 21

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36

<210> 22

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<212> DNA

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21

<210> 23

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<212> DNA

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<400> 23

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24

<210> 24

<211> 24

<212> DNA

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<223> Description of Artificial Sequence: Synthetic Primer

<400> 24

gttgccctga ggatcatccg gaat

24

<210> 25

<211> 30

<212> DNA

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<400> 25
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<210> 26
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<400> 26
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1 5 10

<210> 27
<211> 9
<212> PRT
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<400> 27
Ile Val Glu Pro Asp Thr Glu Ile Lys
1 5

<210> 28
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<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic Peptide

<400> 28
Tyr Gly Phe Ser Pro Arg
1 5

<210> 29
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<220>
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<400> 29
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1 5 10

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 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic Peptide

 <400> 30
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 1 5

<210> 31
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 <213> Rattus rattus

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 1 5

agc ttc ttg gag cag cag gag gcc cgg gac cac cgg aag ggg gca atc	102
Ser Phe Leu Glu Gln Gln Glu Ala Arg Asp His Arg Lys Gly Ala Ile	
10 15 20 25	

ctc gcc cgt gag ttc agc gac att aag gcc cgc tca gtg gct tgg aag	150
Leu Ala Arg Glu Phe Ser Asp Ile Lys Ala Arg Ser Val Ala Trp Lys	
30 35 40	

act gaa ggt gtg tgc tcc act aaa gcc ggc agt cag cag gga aac tca	198
Thr Glu Gly Val Cys Ser Thr Lys Ala Gly Ser Gln Gln Gly Asn Ser	
45 50 55	

aag aag aac cgc tac aaa gac gtg gta ccg tat gat gag acg aga gtc	246
Lys Lys Asn Arg Tyr Lys Asp Val Val Pro Tyr Asp Glu Thr Arg Val	
60 65 70	

atc ctt tcc ctg ctc cag gag gaa gga cac gga gat tac att aat gcc	294
Ile Leu Ser Leu Leu Gln Glu Gly His Gly Asp Tyr Ile Asn Ala	
75 80 85	

aac ttc atc cgg ggc aca gat gga agc cag gcc tac att gcg acg caa	342
Asn Phe Ile Arg Gly Thr Asp Gly Ser Gln Ala Tyr Ile Ala Thr Gln	
90 95 100 105	

gga ccc ctg cct cac act ctg ttg gac ttc tgg cgc ctg gtt tgg gag	390
Gly Pro Leu Pro His Thr Leu Leu Asp Phe Trp Arg Leu Val Trp Glu	
110 115 120	

ttt gga atc aag gtg atc ttg atg gcc tgt cag gag aca gaa aat gga	438
Phe Gly Ile Lys Val Ile Leu Met Ala Cys Gln Glu Thr Glu Asn Gly	
125 130 135	
cg ^g agg aag tgt gaa cgc tac tgg gcc cag gag cg ^g gag cct cta cag	486
Arg Arg Lys Cys Glu Arg Tyr Trp Ala Gln Glu Arg Glu Pro Leu Gln	
140 145 150	
gcc ggg cct ttc tgc atc acc ctg aca aag gag aca gca ctg act tcg	534
Ala Gly Pro Phe Cys Ile Thr Leu Thr Lys Glu Thr Ala Leu Thr Ser	
155 160 165	
gac atc act ctc agg acc ctc cag gtt aca ttc cag aag gaa tcc cgt	582
Asp Ile Thr Leu Arg Thr Leu Gln Val Thr Phe Gln Lys Glu Ser Arg	
170 175 180 185	
cct gtg cac cag cta cag tac atg tct tgg ccg gac cac ggg gtt ccc	630
Pro Val His Gln Leu Gln Tyr Met Ser Trp Pro Asp His Gly Val Pro	
190 195 200	
agc agt tcc gat cac att ctc acc atg gtg gag gag gcc cgt tgc ctc	678
Ser Ser Asp His Ile Leu Thr Met Val Glu Glu Ala Arg Cys Leu	
205 210 215	
caa gga ctt gga cct gga ccc ctc tgt gtc cac tgc agt gct ggc tgt	726
Gln Gly Leu Gly Pro Gly Pro Leu Cys Val His Cys Ser Ala Gly Cys	
220 225 230	
gga cga aca ggt gtc ttg tgt gct gtt gat tac gtg agg cag ttg ctt	774
Gly Arg Thr Gly Val Leu Cys Ala Val Asp Tyr Val Arg Gln Leu Leu	
235 240 245	
ctg act cag aca atc cca ccc aat ttc agc ctc ttt gaa gtg gtc ctg	822
Leu Thr Gln Thr Ile Pro Pro Asn Phe Ser Leu Phe Glu Val Val Leu	
250 255 260 265	
gag atg cg ^g aaa cag cga cct gca gc ^g gtg cag aca gag gag cag tac	870
Glu Met Arg Lys Gln Arg Pro Ala Ala Val Gln Thr Glu Glu Gln Tyr	
270 275 280	
agg ttc ctg tac cac aca gtg gct cag cta ttc tcc cgc act ctc cag	918
Arg Phe Leu Tyr His Thr Val Ala Gln Leu Phe Ser Arg Thr Leu Gln	
285 290 295	
aac aac agt ccc ctc tac cag aac ctc aag gag aac cgc gct cca atc	966
Asn Asn Ser Pro Leu Tyr Gln Asn Leu Lys Glu Asn Arg Ala Pro Ile	
300 305 310	
tgc aag gac tcc tcg tcc ctc agg acc tcc tca gcc ctg cct gcc aca	1014
Cys Lys Asp Ser Ser Leu Arg Thr Ser Ser Ala Leu Pro Ala Thr	
315 320 325	
tcc cgc cca ctg ggt ggc gtt ctc agg agc atc tcg gtg cct ggg cca	1062
Ser Arg Pro Leu Gly Gly Val Leu Arg Ser Ile Ser Val Pro Gly Pro	
330 335 340 345	

ccg acc ctt ccc atg gct gac act tac gct gtg gtg cag aag cgt ggc	1110
Pro Thr Leu Pro Met Ala Asp Thr Tyr Ala Val Val Gln Lys Arg Gly	
350 355 360	
gct tcc ggc agc aca ggg ccg ggc acg cgg gcg ccc aac agc acg gac	1158
Ala Ser Gly Ser Thr Gly Pro Gly Thr Arg Ala Pro Asn Ser Thr Asp	
365 370 375	
acc ccg atc tac agc cag gtg gct cca cgt atc cag cgg ccc gtg tca	1206
Thr Pro Ile Tyr Ser Gln Val Ala Pro Arg Ile Gln Arg Pro Val Ser	
380 385 390	
cac acc gaa aac gcg cag ggg aca acg gca ctg ggc cga gtt cct gcg	1254
His Thr Glu Asn Ala Gln Gly Thr Thr Ala Leu Gly Arg Val Pro Ala	
395 400 405	
gat gaa aac cct tcc ggg cct gat gcc tat gag gaa gta aca gat gga	1302
Asp Glu Asn Pro Ser Gly Pro Asp Ala Tyr Glu Glu Val Thr Asp Gly	
410 415 420 425	
gcg cag act ggt ggg cta ggc ttc aac ttg cgc att gga aga cct aaa	1350
Ala Gln Thr Gly Gly Leu Gly Phe Asn Leu Arg Ile Gly Arg Pro Lys	
430 435 440	
ggg cca cgg gat cct cca gcg gag tgg aca cgg gtg taatgagtgc	1396
Gly Pro Arg Asp Pro Pro Ala Glu Trp Thr Arg Val	
445 450	
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tgtgctgtct tatgtatgag tggactcat gggcctgaat caaaataaaa gtttctcagg	1516
gtagaaaaaa acaaataagg actttggcca gtggttatag cagtcaaagc caggggctag	1576
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caagataccg tctttctcaa aatggaagaa aatagatcct caagaataaa tgtatgtaca	1936
atgctctacg ccctgatcct gccctgcctc actgccataa tgtcacaac aagtcaagggt	1996
ctatatgaca gttgttcatc tagtcagtcc tgactgtggc ctctgcaggc tcagatagtg	2056
ccttctgcag actcttgaa tgcccgctt gaacttgatg aaagcttcta ccgggaacct	2116
gtaaaacatca ttaaaattat taatgtagaa ttcaataaaag agtgggtcaa aaactcaaaa	2176
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<210> 32

<211> 453

<212> PRT

<213> Rattus rattus

<400> 32

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					20			25					30		

Ile	Lys	Ala	Arg	Ser	Val	Ala	Trp	Lys	Thr	Glu	Gly	Val	Cys	Ser	Thr
					35		40					45			

Lys	Ala	Gly	Ser	Gln	Gln	Gly	Asn	Ser	Lys	Lys	Asn	Arg	Tyr	Lys	Asp
				50		55			60						

Val	Val	Pro	Tyr	Asp	Glu	Thr	Arg	Val	Ile	Leu	Ser	Leu	Leu	Gln	Glu
					65		70			75			80		

Glu	Gly	His	Gly	Asp	Tyr	Ile	Asn	Ala	Asn	Phe	Ile	Arg	Gly	Thr	Asp
					85			90				95			

Gly	Ser	Gln	Ala	Tyr	Ile	Ala	Thr	Gln	Gly	Pro	Leu	Pro	His	Thr	Leu
			100				105					110			

Leu	Asp	Phe	Trp	Arg	Leu	Val	Trp	Glu	Phe	Gly	Ile	Lys	Val	Ile	Leu
					115		120				125				

Met	Ala	Cys	Gln	Glu	Thr	Glu	Asn	Gly	Arg	Arg	Lys	Cys	Glu	Arg	Tyr
					130		135			140					

Trp	Ala	Gln	Glu	Arg	Glu	Pro	Leu	Gln	Ala	Gly	Pro	Phe	Cys	Ile	Thr
					145		150			155			160		

Leu	Thr	Lys	Glu	Thr	Ala	Leu	Thr	Ser	Asp	Ile	Thr	Leu	Arg	Thr	Leu
					165			170			175				

Gln	Val	Thr	Phe	Gln	Lys	Glu	Ser	Arg	Pro	Val	His	Gln	Leu	Gln	Tyr
					180		185				190				

Met	Ser	Trp	Pro	Asp	His	Gly	Val	Pro	Ser	Ser	Ser	Asp	His	Ile	Leu
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Thr	Met	Val	Glu	Glu	Ala	Arg	Cys	Leu	Gln	Gly	Leu	Gly	Pro	Gly	Pro
					210		215			220					

Leu	Cys	Val	His	Cys	Ser	Ala	Gly	Cys	Gly	Arg	Thr	Gly	Val	Leu	Cys
					225		230			235			240		

Ala	Val	Asp	Tyr	Val	Arg	Gln	Leu	Leu	Leu	Thr	Gln	Thr	Ile	Pro	Pro
					245			250			255				

Asn	Phe	Ser	Leu	Phe	Glu	Val	Val	Leu	Glu	Met	Arg	Lys	Gln	Arg	Pro
					260		265			270					

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Ala Gln Leu Phe Ser Arg Thr Leu Gln Asn Asn Ser Pro Leu Tyr Gln
 290 295 300

Asn Leu Lys Glu Asn Arg Ala Pro Ile Cys Lys Asp Ser Ser Ser Leu
 305 310 315 320

Arg Thr Ser Ser Ala Leu Pro Ala Thr Ser Arg Pro Leu Gly Gly Val
 325 330 335

Leu Arg Ser Ile Ser Val Pro Gly Pro Pro Thr Leu Pro Met Ala Asp
 340 345 350

Thr Tyr Ala Val Val Gln Lys Arg Gly Ala Ser Gly Ser Thr Gly Pro
 355 360 365

Gly Thr Arg Ala Pro Asn Ser Thr Asp Thr Pro Ile Tyr Ser Gln Val
 370 375 380

Ala Pro Arg Ile Gln Arg Pro Val Ser His Thr Glu Asn Ala Gln Gly
 385 390 395 400

Thr Thr Ala Leu Gly Arg Val Pro Ala Asp Glu Asn Pro Ser Gly Pro
 405 410 415

Asp Ala Tyr Glu Glu Val Thr Asp Gly Ala Gln Thr Gly Gly Leu Gly
 420 425 430

Phe Asn Leu Arg Ile Gly Arg Pro Lys Gly Pro Arg Asp Pro Pro Ala
 435 440 445

Glu Trp Thr Arg Val
 450

<210> 33
 <211> 5581
 <212> DNA
 <213> Unknown Organism

<220>
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 sequence

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 <222> (133) .. (4422)

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 cgacctccaa cc atg gcc cgt gcc cag gcg ctc gtg ctg gca ctc acc ttc 171
 Met Ala Arg Ala Gln Ala Leu Val Leu Ala Leu Thr Phe
 1 5 10

cag ctc tgc gcg ccg gag acc gag act ccg gca gct ggc tgc acc ttc	219
Gln Leu Cys Ala Pro Glu Thr Glu Thr Pro Ala Ala Gly Cys Thr Phe	
15 20 25	
gag gag gca agt gac cca gca gtg ccc tgc gag tac agc cag gcc cag	267
Glu Glu Ala Ser Asp Pro Ala Val Pro Cys Glu Tyr Ser Gln Ala Gln	
30 35 40 45	
tac gat gac ttc cag tgg gag caa gtg cga atc cac cct ggc acc cgg	315
Tyr Asp Asp Phe Gln Trp Glu Gln Val Arg Ile His Pro Gly Thr Arg	
50 55 60	
gca cct gcg gac ctg ccc cac ggc tcc tac ttg atg gtc aac act tcc	363
Ala Pro Ala Asp Leu Pro His Gly Ser Tyr Leu Met Val Asn Thr Ser	
65 70 75	
cag cat gcc cca ggc cag cga gac cat gtc atc ttc cag agc ctg agc	411
Gln His Ala Pro Gly Gln Arg Ala His Val Ile Phe Gln Ser Leu Ser	
80 85 90	
gag aat gat acc cac tgt gtg cag ttc agc tac ttc ctg tac agc cgg	459
Glu Asn Asp Thr His Cys Val Gln Phe Ser Tyr Phe Leu Tyr Ser Arg	
95 100 105	
gac ggc aca ggc acc ctg cgc gtc tac gtg cgc gtt aat ggg ggc	507
Asp Gly Thr Gly Thr Leu Arg Val Tyr Val Arg Val Asn Gly Gly	
110 115 120 125	
ccc ctg gcg agt gct gtg tgg aat atg act gga tcc cac ggc cgt cag	555
Pro Leu Ala Ser Ala Val Trp Asn Met Thr Gly Ser His Gly Arg Gln	
130 135 140	
tgg cac cag gct gag ctg gct gtc agc act ttc tgg ccc aat gaa tat	603
Trp His Gln Ala Glu Leu Ala Val Ser Thr Phe Trp Pro Asn Glu Tyr	
145 150 155	
cag gtg ctg ttt gag gcc ctc atc tcc cca gac cgc agg ggc tac atg	651
Gln Val Leu Phe Glu Ala Leu Ile Ser Pro Asp Arg Arg Gly Tyr Met	
160 165 170	
ggc cta gat gac atc ctg ctt ctc agc tac ccc tgc gca aag gcc cca	699
Gly Leu Asp Asp Ile Leu Leu Ser Tyr Pro Cys Ala Lys Ala Pro	
175 180 185	
cac ttc tcc cgc ctg ggc gac gtg gag gtc aac gcg ggc cag aac gcg	747
His Phe Ser Arg Leu Gly Asp Val Glu Val Asn Ala Gly Gln Asn Ala	
190 195 200 205	
tcg ttc cag tgc atg gcc gcg gga gag ccc atg cgc caa cgc ttc ctc	795
Ser Phe Gln Cys Met Ala Ala Gly Glu Pro Met Arg Gln Arg Phe Leu	
210 215 220	
ttg caa cgg caq agc qgg gcc ctg gtg ccg gcc qgg gcg ttc ggc aca	843
Leu Gln Arg Gln Ser Gly Ala Leu Val Pro Ala Gly Ala Phe Gly Thr	
225 230 235	

tca gcc acc ggc ttc ctg gcc act ttc ccg ctg gct gcc gtg agc cgc	891
Ser Ala Thr Gly Phe Leu Ala Thr Phe Pro Leu Ala Ala Val Ser Arg	
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gcc gag cag gac ctg tac cgc tgt gtg tcc cag gcc ccg cgc ggc ggc	939
Ala Glu Gln Asp Leu Tyr Arg Cys Val Ser Gln Ala Pro Arg Gly Gly	
255 260 265	
gtc tct aac ttc ccg gag ctc atc gtc aag gag ccc cca act ccc atc	987
Val Ser Asn Phe Pro Glu Leu Ile Val Lys Glu Pro Pro Thr Pro Ile	
270 275 280 285	
gcg ccc cca cag ctg ctg cgt gct ggc ccc acc tac ctc atc atc cag	1035
Ala Pro Pro Gln Leu Leu Arg Ala Gly Pro Thr Tyr Leu Ile Ile Gln	
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ctc aac acc aac tcc atc att ggc gac ggg ccg atc gtg cgc aag gag	1083
Leu Asn Thr Asn Ser Ile Ile Gly Asp Gly Pro Ile Val Arg Lys Glu	
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att gag tac cgc atg gcg cgc ggg ccc tgg gct gag gtg cac gcc gtc	1131
Ile Glu Tyr Arg Met Ala Arg Gly Pro Trp Ala Glu Val His Ala Val	
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agc ctg cag acc tac aag ctg tgg cac ctc gac ccc gac aca gac tat	1179
Ser Leu Gln Thr Tyr Lys Leu Trp His Leu Asp Pro Asp Thr Asp Tyr	
335 340 345	
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Glu Ile Ser Val Leu Leu Thr Arg Pro Gly Asp Gly Gly Thr Gly Arg	
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tgg gcc acc cct cat cag ccg cac caa atg cgc aga gcc cat gag ggc	1275
Trp Ala Thr Pro His Gln Pro His Gln Met Arg Arg Ala His Glu Gly	
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ccc aaa ggc ctg gct ttt gct gag atc cag gcc cgt cag ctg acc ctg	1323
Pro Lys Gly Leu Ala Phe Ala Glu Ile Gln Ala Arg Gln Leu Thr Leu	
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cag tgg gaa cca ctg ggc tac aac gtg acg cgt tgc cac acc tat act	1371
Gln Trp Glu Pro Leu Gly Tyr Asn Val Thr Arg Cys His Thr Tyr Thr	
400 405 410	
gtg tcg ctg tgc tat cac tac acc ctg ggc agc agc cac aac cag acc	1419
Val Ser Leu Cys Tyr His Tyr Thr Leu Gly Ser Ser His Asn Gln Thr	
415 420 425	
atc cga gag tgt gtg aag aca gag caa ggt gtc agc cgc tac acc atc	1467
Ile Arg Glu Cys Val Lys Thr Glu Gln Gly Val Ser Arg Tyr Thr Ile	
430 435 440 445	
aag aac ctg ctg ccc tat cgg aac gtt cac gtg agg ctt gtc ctc act	1515
Lys Asn Leu Leu Pro Tyr Arg Asn Val His Val Arg Leu Val Leu Thr	
450 455 460	

aac cct gag ggg cgc aaa gag ggc aag gag gtc act ttc cag acg gat		1563	
Asn Pro Glu Gly Arg Lys Glu Gly Lys Glu Val Thr Phe Gln Thr Asp			
465	470	475	
gag gat gtg ccc agt ggg att gca gcc gag tcc ctg acc ttc act cca		1611	
Glu Asp Val Pro Ser Gly Ile Ala Ala Glu Ser Leu Thr Phe Thr Pro			
480	485	490	
ctg gag gac atg atc ttc ctc aag tgg gag gag ccc cag gag ccc aat		1659	
Leu Glu Asp Met Ile Phe Leu Lys Trp Glu Glu Pro Gln Glu Pro Asn			
495	500	505	
ggt ctc atc acc cag tat gag atc agc tac cag agc atc gag tca tca		1707	
Gly Leu Ile Thr Gln Tyr Glu Ile Ser Tyr Gln Ser Ile Glu Ser Ser			
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gac ccg gca gtg aac gtg cca ggc cca cga cgt acc atc tcc aag ctc		1755	
Asp Pro Ala Val Asn Val Pro Gly Pro Arg Arg Thr Ile Ser Lys Leu			
530	535	540	
cgc aat gag acc tac cat gtc ttc tcc aac ctg cac cca ggc acc acc		1803	
Arg Asn Glu Thr Tyr His Val Phe Ser Asn Leu His Pro Gly Thr Thr			
545	550	555	
tac ctg ttc tcc gtg cgg gcc cgc aca ggc aaa ggc ttc ggc cag gcg		1851	
Tyr Leu Phe Ser Val Arg Ala Arg Thr Gly Lys Gly Phe Gly Gln Ala			
560	565	570	
gca ctc act gag ata acc act aac atc tct gct ccc agc ttt gat tat		1899	
Ala Leu Thr Glu Ile Thr Asn Ile Ser Ala Pro Ser Phe Asp Tyr			
575	580	585	
gcc gac atg ccg tca ccc ctg ggc gag tct gag aac acc atc acc gtg		1947	
Ala Asp Met Pro Ser Pro Leu Gly Glu Ser Glu Asn Thr Ile Thr Val			
590	595	600	605
ctg ctg agg ccg gca cag ggc cgc ggt gcg ccc atc agt gtg tac cag		1995	
Leu Leu Arg Pro Ala Gln Gly Arg Gly Ala Pro Ile Ser Val Tyr Gln			
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gtg att gtg gag gag gag cgg gcg cga ggc tgc ggc ggg acg agg tgg		2043	
Val Ile Val Glu Glu Arg Ala Arg Gly Cys Gly Gly Thr Arg Trp			
625	630	635	
aca gga ctg ctt ccc agt gcc att gac ctt cga ggc ggc gct ggc ccc		2091	
Thr Gly Leu Leu Pro Ser Ala Ile Asp Leu Arg Gly Gly Ala Gly Pro			
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agg ctg gtg cac tac ttc ggg gcc gaa ctg gcg gcc agc agt cta cct		2139	
Arg Leu Val His Tyr Phe Gly Ala Glu Leu Ala Ala Ser Ser Leu Pro			
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gag gcc atg ccc ttt acc gtg ggt gac aac cag acc tac cga ggc ttc		2187	
Glu Ala Met Pro Phe Thr Val Gly Asp Asn Gln Thr Tyr Arg Gly Phe			
670	675	680	685

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Trp Asn Pro Pro Leu Glu Pro Arg Lys Ala Tyr Leu Ile Tyr Phe Gln	
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gca gca agc cac ctg aag ggg gag acc cgg ctg aat tgc atc cgc att	2283
Ala Ala Ser His Leu Lys Gly Glu Thr Arg Leu Asn Cys Ile Arg Ile	
705 710 715	
gcc agg aaa gct gcc tgc aag gaa agc aag cgg ccc ctg gag gtg tcc	2331
Ala Arg Lys Ala Ala Cys Lys Glu Ser Lys Arg Pro Leu Glu Val Ser	
720 725 730	
cag aga tcg gag gag atg ggg ctt atc ctg ggc atc tgt gca ggg ggg	2379
Gln Arg Ser Glu Glu Met Gly Leu Ile Leu Gly Ile Cys Ala Gly Gly	
735 740 745	
ctt gct gtc ctc atc ctt ctc ctg ggt gcc atc att gtc atc atc cgc	2427
Leu Ala Val Leu Ile Leu Leu Gly Ala Ile Ile Val Ile Ile Arg	
750 755 760 765	
aaa ggg aag ccg gtg aac atg acc aag gcc acc gtc aac tac cgc cag	2475
Lys Gly Lys Pro Val Asn Met Thr Lys Ala Thr Val Asn Tyr Arg Gln	
770 775 780	
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Glu Lys Thr His Met Ile Ser Ala Val Asp Arg Ser Phe Thr Asp Gln	
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agc acc ctg cag gag gac gag cgg ctg ggc ctg tcc ttc atg gac acc	2571
Ser Thr Leu Gln Glu Asp Glu Arg Leu Gly Leu Ser Phe Met Asp Thr	
800 805 810	
cat ggc tac agc acc cgg gga gac cag cgc agc ggt ggg gtc act gag	2619
His Gly Tyr Ser Thr Arg Gly Asp Gln Arg Ser Gly Gly Val Thr Glu	
815 820 825	
gcc agc agc ctc ctg ggg ggc tcc ccg agg cgt ccc tgt ggc cgg aag	2667
Ala Ser Ser Leu Leu Gly Gly Ser Pro Arg Arg Pro Cys Gly Arg Lys	
830 835 840 845	
ggc tcc cca tac cac acg ggg cag ctg cac cct gcg gtg cgt gtc gca	2715
Gly Ser Pro Tyr His Thr Gly Gln Leu His Pro Ala Val Arg Val Ala	
850 855 860	
gac ctt ctg cag cac atc aac cag atg aag acg gcc gag ggt tac ggc	2763
Asp Leu Leu Gln His Ile Asn Gln Met Lys Thr Ala Glu Gly Tyr Gly	
865 870 875	
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Phe Lys Gln Glu Tyr Glu Ser Phe Phe Glu Gly Trp Asp Ala Thr Lys	
880 885 890	
aag aaa gac aag gtc aag ggc agc cgg cag gag cca atg cct gcc tat	2859
Lys Lys Asp Lys Val Lys Gly Ser Arg Gln Glu Pro Met Pro Ala Tyr	
895 900 905	

gat	cg	cac	cga	gtg	aaa	ctg	cac	ccg	atg	ctg	gga	gac	ccc	aat	gcc	2907
Asp	Arg	His	Arg	Val	Lys	Leu	His	Pro	Met	Leu	Gly	Asp	Pro	Asn	Ala	
910					915					920					925	
gac	tac	att	aat	gcc	aac	tac	ata	gat	ggt	tac	cac	agg	tca	aac	cac	2955
Asp	Tyr	Ile	Asn	Ala	Asn	Tyr	Ile	Asp	Gly	Tyr	His	Arg	Ser	Asn	His	
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ttc	ata	gcc	act	caa	ggg	ccg	aag	cct	gag	atg	gtc	tat	gac	ttc	tgg	3003
Phe	Ile	Ala	Thr	Gln	Gly	Pro	Lys	Pro	Glu	Met	Val	Tyr	Asp	Phe	Trp	
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cgt	atg	gtg	tgg	cag	gag	cac	tgt	tcc	agc	atc	gtc	atg	atc	acc	aag	3051
Arg	Met	Val	Trp	Gln	Glu	His	Cys	Ser	Ser	Ile	Val	Met	Ile	Thr	Lys	
960					965					970						
ctg	gtc	gag	gtg	ggc	agg	gtg	aaa	tgc	tca	cg	tac	tgg	ccg	gag	gac	3099
Leu	Val	Glu	Val	Gly	Arg	Val	Lys	Cys	Ser	Arg	Tyr	Trp	Pro	Glu	Asp	
975					980					985						
tca	gac	acc	tac	ggg	gac	atc	aag	att	atg	ctg	gtg	aag	aca	gag	acc	3147
Ser	Asp	Thr	Tyr	Gly	Asp	Ile	Lys	Ile	Met	Leu	Val	Lys	Thr	Glu	Thr	
990					995					1000				1005		
ctg	gct	gag	tat	gtc	gtg	cgc	act	ttt	gcc	ctg	gag	cg	aga	ggc	tac	3195
Leu	Ala	Glu	Tyr	Val	Val	Arg	Thr	Phe	Ala	Leu	Glu	Arg	Arg	Gly	Tyr	
1010					1015					1020						
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Ser	Ala	Arg	His	Glu	Val	Arg	Gln	Ser	His	Phe	Thr	Ala	Trp	Pro	Glu	
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cat	ggc	gtc	ccc	tac	cat	gcc	acg	ggg	ctg	ctg	gct	ttc	atc	cg	cg	3291
His	Gly	Val	Pro	Tyr	His	Ala	Thr	Gly	Leu	Leu	Ala	Phe	Ile	Arg	Arg	
1040					1045					1050						
gtg	aag	ggc	tcc	acc	cca	cct	gat	gcc	ggg	ccc	att	gtc	atc	ca	tgc	3339
Val	Lys	Ala	Ser	Thr	Pro	Pro	Asp	Ala	Gly	Pro	Ile	Val	Ile	His	Cys	
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Ser	Ala	Gly	Thr	Gly	Arg	Thr	Arg	Cys	Tyr	Ile	Val	Leu	Asp	Val	Met	
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ctg	gac	atg	gca	gag	tgt	gag	ggc	gtc	gtg	gac	att	tac	aac	tgt	gtg	3435
Leu	Asp	Met	Ala	Glu	Cys	Glu	Gly	Val	Val	Asp	Ile	Tyr	Asn	Cys	Val	
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aag	act	ctc	tgc	tcc	cg	cgt	gtc	aac	atg	atc	cag	act	gag	gag	cag	3483
Lys	Thr	Leu	Cys	Ser	Arg	Arg	Val	Asn	Met	Ile	Gln	Thr	Glu	Glu	Gln	
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tac	atc	ttc	att	cat	gat	gca	atc	ctg	gag	ggc	tgc	ctg	tgt	ggg	gag	3531
Tyr	Ile	Phe	Ile	His	Asp	Ala	Ile	Leu	Glu	Ala	Cys	Leu	Cys	Gly	Glu	
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Thr Thr Ile Pro Val Ser Glu Phe Lys Ala Thr Tyr Lys Glu Met Ile	
1135 1140 1145	
cgc att gat cct cag agt aat tcc tcc cag ctg cg gaa gag ttc cag	3627
Arg Ile Asp Pro Gln Ser Asn Ser Gln Leu Arg Glu Glu Phe Gln	
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acg ctg aac tcg gtc acc ccg ctg gac gtg gag gag tgc agc atc	3675
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1170 1175 1180	
gcc ctg ttg ccc cg aac cg cgc gac aag aac cg cgc agc atg gac gtc ctg	3723
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Ala Phe Met Val Thr Leu His Pro Leu Gln Ser Thr Thr Pro Asp Phe	
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Trp Arg Leu Val Tyr Asp Tyr Gly Cys Thr Ser Ile Val Met Leu Asn	
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cag ctg aac cg tcc aac tcc gcc tgg ccc tgc ctg cag tac tgg cca	3963
Gln Leu Asn Gln Ser Asn Ser Ala Trp Pro Cys Leu Gln Tyr Trp Pro	
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gag cca ggc cg cag caa tat ggc ctc atg gag gtg gag ttt atg tcg	4011
Glu Pro Gly Arg Gln Gln Tyr Gly Leu Met Glu Val Glu Phe Met Ser	
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Gly Thr Ala Asp Glu Asp Leu Val Ala Arg Val Phe Arg Val Gln Asn	
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Ile Ser Arg Leu Gln Glu Gly Asp Leu Leu Val Arg His Phe Gln Phe	
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ctg cgc tgg tct gca tac cg gac aca cct gac tcc aag aag gcc ttc	4155
Leu Arg Trp Ser Ala Tyr Arg Asp Thr Pro Asp Ser Lys Lys Ala Phe	
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ttg cac ctg ctg gct gag gtg gac aag tgg cag gcc gag agt ggg gat	4203
Leu His Leu Leu Ala Glu Val Asp Lys Trp Gln Ala Glu Ser Gly Asp	
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ggg cgc acc atc gtg cac tgc cta aac ggg gga gga cgc agc ggc acc	4251
Gly Arg Thr Ile Val His Cys Leu Asn Gly Gly Arg Ser Gly Thr	
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Phe Cys Ala Cys Ala Thr Val Leu Glu Met Ile Arg Cys His Asn Leu	
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Val Asp Val Phe Phe Ala Ala Gln Thr Leu Arg Asn Tyr Lys Pro Asn	
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<210> 34

<211> 1430

<212> PRT

<213> Unknown Organism

<223> Description of Unknown Organism: Mammalian PCP-2 sequence

<400> 34

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Ala	Pro	Glu	Thr	Glu	Thr	Pro	Ala	Ala	Gly	Cys	Thr	Phe	Glu	Glu	Ala
							20		25				30		

Ser	Asp	Pro	Ala	Val	Pro	Cys	Glu	Tyr	Ser	Gln	Ala	Gln	Tyr	Asp	Asp
							35		40			45			

Phe	Gln	Trp	Glu	Gln	Val	Arg	Ile	His	Pro	Gly	Thr	Arg	Ala	Pro	Ala
					50		55			60					

Asp	Leu	Pro	His	Gly	Ser	Tyr	Leu	Met	Val	Asn	Thr	Ser	Gln	His	Ala
					65		70			75			80		

Pro	Gly	Gln	Arg	Ala	His	Val	Ile	Phe	Gln	Ser	Leu	Ser	Glu	Asn	Asp
					85			90			95				

Thr	His	Cys	Val	Gln	Phe	Ser	Tyr	Phe	Leu	Tyr	Ser	Arg	Asp	Gly	Thr
					100			105			110				

Gly	Gly	Thr	Leu	Arg	Val	Tyr	Val	Arg	Val	Asn	Gly	Gly	Pro	Leu	Ala
					115		120			125					

Ser	Ala	Val	Trp	Asn	Met	Thr	Gly	Ser	His	Gly	Arg	Gln	Trp	His	Gln
					130		135			140					

Ala	Glu	Leu	Ala	Val	Ser	Thr	Phe	Trp	Pro	Asn	Glu	Tyr	Gln	Val	Leu
					145		150			155			160		

Phe	Glu	Ala	Leu	Ile	Ser	Pro	Asp	Arg	Arg	Gly	Tyr	Met	Gly	Leu	Asp
						165		170			175				

Asp	Ile	Leu	Leu	Leu	Ser	Tyr	Pro	Cys	Ala	Lys	Ala	Pro	His	Phe	Ser
					180			185			190				

Arg	Leu	Gly	Asp	Val	Glu	Val	Asn	Ala	Gly	Gln	Asn	Ala	Ser	Phe	Gln
					195		200			205					

Cys	Met	Ala	Ala	Gly	Glu	Pro	Met	Arg	Gln	Arg	Phe	Leu	Leu	Gln	Arg
					210		215			220					

Gln	Ser	Gly	Ala	Leu	Val	Pro	Ala	Gly	Ala	Phe	Gly	Thr	Ser	Ala	Thr
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Gly	Phe	Leu	Ala	Thr	Phe	Pro	Leu	Ala	Ala	Val	Ser	Arg	Ala	Glu	Gln
					245			250			255				

Asp Leu Tyr Arg Cys Val Ser Gln Ala Pro Arg Gly Gly Val Ser Asn
 260 265 270

Phe Pro Glu Leu Ile Val Lys Glu Pro Pro Thr Pro Ile Ala Pro Pro
 275 280 285

Gln Leu Leu Arg Ala Gly Pro Thr Tyr Leu Ile Ile Gln Leu Asn Thr
 290 295 300

Asn Ser Ile Ile Gly Asp Gly Pro Ile Val Arg Lys Glu Ile Glu Tyr
 305 310 315 320

Arg Met Ala Arg Gly Pro Trp Ala Glu Val His Ala Val Ser Leu Gln
 325 330 335

Thr Tyr Lys Leu Trp His Leu Asp Pro Asp Thr Asp Tyr Glu Ile Ser
 340 345 350

Val Leu Leu Thr Arg Pro Gly Asp Gly Gly Thr Gly Arg Trp Ala Thr
 355 360 365

Pro His Gln Pro His Gln Met Arg Arg Ala His Glu Gly Pro Lys Gly
 370 375 380

Leu Ala Phe Ala Glu Ile Gln Ala Arg Gln Leu Thr Leu Gln Trp Glu
 385 390 395 400

Pro Leu Gly Tyr Asn Val Thr Arg Cys His Thr Tyr Thr Val Ser Leu
 405 410 415

Cys Tyr His Tyr Thr Leu Gly Ser Ser His Asn Gln Thr Ile Arg Glu
 420 425 430

Cys Val Lys Thr Glu Gln Gly Val Ser Arg Tyr Thr Ile Lys Asn Leu
 435 440 445

Leu Pro Tyr Arg Asn Val His Val Arg Leu Val Leu Thr Asn Pro Glu
 450 455 460

Gly Arg Lys Glu Gly Lys Glu Val Thr Phe Gln Thr Asp Glu Asp Val
 465 470 475 480

Pro Ser Gly Ile Ala Ala Glu Ser Leu Thr Phe Thr Pro Leu Glu Asp
 485 490 495

Met Ile Phe Leu Lys Trp Glu Glu Pro Gln Glu Pro Asn Gly Leu Ile
 500 505 510

Thr Gln Tyr Glu Ile Ser Tyr Gln Ser Ile Glu Ser Ser Asp Pro Ala
 515 520 525

Val Asn Val Pro Gly Pro Arg Arg Thr Ile Ser Lys Leu Arg Asn Glu
 530 535 540

Thr Tyr His Val Phe Ser Asn Leu His Pro Gly Thr Thr Tyr Leu Phe
 545 550 555 560

Ser Val Arg Ala Arg Thr Gly Lys Gly Phe Gly Gln Ala Ala Leu Thr
 565 570 575

Glu Ile Thr Thr Asn Ile Ser Ala Pro Ser Phe Asp Tyr Ala Asp Met
 580 585 590

Pro Ser Pro Leu Gly Glu Ser Glu Asn Thr Ile Thr Val Leu Leu Arg
 595 600 605

Pro Ala Gln Gly Arg Gly Ala Pro Ile Ser Val Tyr Gln Val Ile Val
 610 615 620

Glu Glu Glu Arg Ala Arg Gly Cys Gly Thr Arg Trp Thr Gly Leu
 625 630 635 640

Leu Pro Ser Ala Ile Asp Leu Arg Gly Gly Ala Gly Pro Arg Leu Val
 645 650 655

His Tyr Phe Gly Ala Glu Leu Ala Ala Ser Ser Leu Pro Glu Ala Met
 660 665 670

Pro Phe Thr Val Gly Asp Asn Gln Thr Tyr Arg Gly Phe Trp Asn Pro
 675 680 685

Pro Leu Glu Pro Arg Lys Ala Tyr Leu Ile Tyr Phe Gln Ala Ala Ser
 690 695 700

His Leu Lys Gly Glu Thr Arg Leu Asn Cys Ile Arg Ile Ala Arg Lys
 705 710 715 720

Ala Ala Cys Lys Glu Ser Lys Arg Pro Leu Glu Val Ser Gln Arg Ser
 725 730 735

Glu Glu Met Gly Leu Ile Leu Gly Ile Cys Ala Gly Gly Leu Ala Val
 740 745 750

Leu Ile Leu Leu Gly Ala Ile Ile Val Ile Ile Arg Lys Gly Lys
 755 760 765

Pro Val Asn Met Thr Lys Ala Thr Val Asn Tyr Arg Gln Glu Lys Thr
 770 775 780

His Met Ile Ser Ala Val Asp Arg Ser Phe Thr Asp Gln Ser Thr Leu
 785 790 795 800

Gln Glu Asp Glu Arg Leu Gly Leu Ser Phe Met Asp Thr His Gly Tyr
 805 810 815

Ser Thr Arg Gly Asp Gln Arg Ser Gly Gly Val Thr Glu Ala Ser Ser
 820 825 830

Leu Leu Gly Gly Ser Pro Arg Arg Pro Cys Gly Arg Lys Gly Ser Pro
 835 840 845

Tyr His Thr Gly Gln Leu His Pro Ala Val Arg Val Ala Asp Leu Leu
 850 855 860

Gln His Ile Asn Gln Met Lys Thr Ala Glu Gly Tyr Gly Phe Lys Gln
 865 870 875 880

Glu Tyr Glu Ser Phe Phe Glu Gly Trp Asp Ala Thr Lys Lys Lys Asp
 885 890 895

Lys Val Lys Gly Ser Arg Gln Glu Pro Met Pro Ala Tyr Asp Arg His
 900 905 910

Arg Val Lys Leu His Pro Met Leu Gly Asp Pro Asn Ala Asp Tyr Ile
 915 920 925

Asn Ala Asn Tyr Ile Asp Gly Tyr His Arg Ser Asn His Phe Ile Ala
 930 935 940

Thr Gln Gly Pro Lys Pro Glu Met Val Tyr Asp Phe Trp Arg Met Val
 945 950 955 960

Trp Gln Glu His Cys Ser Ser Ile Val Met Ile Thr Lys Leu Val Glu
 965 970 975

Val Gly Arg Val Lys Cys Ser Arg Tyr Trp Pro Glu Asp Ser Asp Thr
 980 985 990

Tyr Gly Asp Ile Lys Ile Met Leu Val Lys Thr Glu Thr Leu Ala Glu
 995 1000 1005

Tyr Val Val Arg Thr Phe Ala Leu Glu Arg Arg Gly Tyr Ser Ala Arg
 1010 1015 1020

His Glu Val Arg Gln Ser His Phe Thr Ala Trp Pro Glu His Gly Val
 1025 1030 1035 1040

Pro Tyr His Ala Thr Gly Leu Ala Phe Ile Arg Arg Val Lys Ala
 1045 1050 1055

Ser Thr Pro Pro Asp Ala Gly Pro Ile Val Ile His Cys Ser Ala Gly
 1060 1065 1070

Thr Gly Arg Thr Arg Cys Tyr Ile Val Leu Asp Val Met Leu Asp Met
 1075 1080 1085

Ala Glu Cys Glu Gly Val Val Asp Ile Tyr Asn Cys Val Lys Thr Leu
 1090 1095 1100

Cys Ser Arg Arg Val Asn Met Ile Gln Thr Glu Glu Gln Tyr Ile Phe
 1105 1110 1115 1120

Ile His Asp Ala Ile Leu Glu Ala Cys Leu Cys Gly Glu Thr Thr Ile
 1125 1130 1135

Pro Val Ser Glu Phe Lys Ala Thr Tyr Lys Glu Met Ile Arg Ile Asp
 1140 1145 1150

Pro Gln Ser Asn Ser Ser Gln Leu Arg Glu Glu Phe Gln Thr Leu Asn
 1155 1160 1165

Ser Val Thr Pro Pro Leu Asp Val Glu Glu Cys Ser Ile Ala Leu Leu
 1170 1175 1180

Pro Arg Asn Arg Asp Lys Asn Arg Ser Met Asp Val Leu Pro Pro Asp
 1185 1190 1195 1200

Arg Cys Leu Pro Phe Leu Ile Ser Thr Asp Gly Asp Ser Asn Asn Tyr
 1205 1210 1215

Ile Asn Ala Ala Leu Thr Asp Ser Tyr Thr Arg Arg Ser Ala Phe Met
 1220 1225 1230

Val Thr Leu His Pro Leu Gln Ser Thr Thr Pro Asp Phe Trp Arg Leu
 1235 1240 1245

Val Tyr Asp Tyr Gly Cys Thr Ser Ile Val Met Leu Asn Gln Leu Asn
 1250 1255 1260

Gln Ser Asn Ser Ala Trp Pro Cys Leu Gln Tyr Trp Pro Glu Pro Gly
 1265 1270 1275 1280

Arg Gln Gln Tyr Gly Leu Met Glu Val Glu Phe Met Ser Gly Thr Ala
 1285 1290 1295

Asp Glu Asp Leu Val Ala Arg Val Phe Arg Val Gln Asn Ile Ser Arg
 1300 1305 1310

Leu Gln Glu Gly Asp Leu Leu Val Arg His Phe Gln Phe Leu Arg Trp
 1315 1320 1325

Ser Ala Tyr Arg Asp Thr Pro Asp Ser Lys Lys Ala Phe Leu His Leu
 1330 1335 1340

Leu Ala Glu Val Asp Lys Trp Gln Ala Glu Ser Gly Asp Gly Arg Thr
 1345 1350 1355 1360

Ile Val His Cys Leu Asn Gly Gly Arg Ser Gly Thr Phe Cys Ala
 1365 1370 1375

Cys Ala Thr Val Leu Glu Met Ile Arg Cys His Asn Leu Val Asp Val
 1380 1385 1390

Phe Phe Ala Ala Gln Thr Leu Arg Asn Tyr Lys Pro Asn Met Val Glu
 1395 1400 1405

Thr Met Asp Gln Tyr His Phe Cys Tyr Asp Val Ala Leu Glu Tyr Leu
 1410 1415 1420

Glu Gly Leu Glu Ser Arg
 1425 1430

<210> 35
 <211> 2810
 <212> DNA
 <213> Homo sapiens

<220>
<221> CDS
<222> (44)..(1417)

<400> 35
gaattcggca cgagcgggct ggaccttgct cgcccgcgcc gcc atg agc cgc agc 55
Met Ser Arg Ser
1

ctg gac tcg gcg cgg agc ttc ctg gag cgg ctg gaa gcg cgg ggc ggc 103
Leu Asp Ser Ala Arg Ser Phe Leu Glu Arg Leu Glu Ala Arg Gly Gly
5 10 15 20

cg gag ggg gca gtc ctc gcc ggc gag ttc agc gac atc cag gcc tgc 151
Arg Glu Gly Ala Val Leu Ala Gly Glu Phe Ser Asp Ile Gln Ala Cys
25 30 35

tcg gcc gcc tgg aag gct gac ggc gtg tgc tcc acc gtg gcc ggc agt 199
Ser Ala Ala Trp Lys Ala Asp Gly Val Cys Ser Thr Val Ala Gly Ser
40 45 50

cgg cca gag aac gtg agg aag aac cgc tac aaa gac gtg ctg cct tat 247
Arg Pro Glu Asn Val Arg Lys Asn Arg Tyr Lys Asp Val Leu Pro Tyr
55 60 65

gat cag acg cga gta atc ctc tcc ctg ctc cag gaa gag gga cac agc 295
Asp Gln Thr Arg Val Ile Leu Ser Leu Leu Gln Glu Glu Gly His Ser
70 75 80

gac tac att aat ggc aac ttc atc cgg ggc gtg gat gga agc ctg gcc 343
Asp Tyr Ile Asn Gly Asn Phe Ile Arg Gly Val Asp Gly Ser Leu Ala
85 90 95 100

tac att gcc acg caa gga ccc ttg cct cac acc ctg cta gac ttc tgg 391
Tyr Ile Ala Thr Gln Gly Pro Leu Pro His Thr Leu Leu Asp Phe Trp
105 110 115

aga ctg gtc tgg gag ttt ggg gtc aag gtg atc ctg atg gcc tgt cga 439
Arg Leu Val Trp Glu Phe Gly Val Lys Val Ile Leu Met Ala Cys Arg
120 125 130

gag ata gag aat ggg cgg aaa agg tgt gag cgg tac tgg gcc cag gag 487
Glu Ile Glu Asn Gly Arg Lys Arg Cys Glu Arg Tyr Trp Ala Gln Glu
135 140 145

cag gag cca ctg cag act ggg ctt ttc tgc atc act ctg ata aag gag 535
Gln Glu Pro Leu Gln Thr Gly Leu Phe Cys Ile Thr Leu Ile Lys Glu
150 155 160

aag tgg ctg aat gag gac atc atg ctc agg acc ctc aag gtc aca ttc 583
Lys Trp Leu Asn Glu Asp Ile Met Leu Arg Thr Leu Lys Val Thr Phe
165 170 175 180

cag aag gag tcc cgt tct gtg tac cag cta cag tat atg tcc tgg cca 631
Gln Lys Glu Ser Arg Ser Val Tyr Gln Leu Gln Tyr Met Ser Trp Pro
185 190 195

gac cgt ggg gtc ccc agc agt cct gac cac atg ctc gcc atg gtg gag 679

Asp Arg Gly Val Pro Ser Ser Pro Asp His Met Leu Ala Met Val Glu			
200	205	210	
gaa gcc cgt cgc ctc cag gga tct ggc cct gaa ccc ctc tgt gtc cac		727	
Glu Ala Arg Arg Leu Gln Gly Ser Gly Pro Glu Pro Leu Cys Val His			
215	220	225	
tgc agt gct ggt tgt ggg cga aca ggc gtc ctg tgc acc gtg gat tat		775	
Cys Ser Ala Gly Cys Gly Arg Thr Gly Val Leu Cys Thr Val Asp Tyr			
230	235	240	
gtg agg cag ctg ctc ctg acc cag atg atc cca cct gac ttc agt ctc		823	
Val Arg Gln Leu Leu Thr Gln Met Ile Pro Pro Asp Phe Ser Leu			
245	250	255	260
ttt gat gtg gtc ctt aag atg agg aag cag cgg cct gct gcc gtg cag		871	
Phe Asp Val Val Leu Lys Met Arg Lys Gln Arg Pro Ala Ala Val Gln			
265	270	275	
aca gag gag cag tac agg ttc ctg tac cac acg gtg gct cag atg ttc		919	
Thr Glu Glu Gln Tyr Arg Phe Leu Tyr His Thr Val Ala Gln Met Phe			
280	285	290	
tgc tcc aca ctc cag aat gcc agc ccc cac tac cag aac atc aaa gag		967	
Cys Ser Thr Leu Gln Asn Ala Ser Pro His Tyr Gln Asn Ile Lys Glu			
295	300	305	
aat tgt gcc cca ctc tac gac gat gcc ctc ttc ctc cgg act ccc cag		1015	
Asn Cys Ala Pro Leu Tyr Asp Asp Ala Leu Phe Leu Arg Thr Pro Gln			
310	315	320	
gca ctt ctc gcc ata ccc cgc cca cca gga ggg gtc ctc agg agc atc		1063	
Ala Leu Leu Ala Ile Pro Arg Pro Gly Gly Val Leu Arg Ser Ile			
325	330	335	340
tct gtg ccc ggg tcc ccg ggc cac gcc atg gct gac acc tac gct gag		1111	
Ser Val Pro Gly Ser Pro Gly His Ala Met Ala Asp Thr Tyr Ala Glu			
345	350	355	
gag cag aag cgc ggg gct cca gcg ggc gcc ggg agt ggg acg cag acg		1159	
Glu Gln Lys Arg Gly Ala Pro Ala Gly Ala Gly Ser Gly Thr Gln Thr			
360	365	370	
ggg acg ggg acg ggg gcg cgc agc gct gag gac ggg ccc ctc tac agc		1207	
Gly Thr Gly Thr Gly Ala Arg Ser Ala Glu Glu Ala Pro Leu Tyr Ser			
375	380	385	
aag gtg acg ccg cgc gcc cag cga ccc ggg gcg cac gct gag gac gct		1255	
Lys Val Thr Pro Arg Ala Gln Arg Pro Gly Ala His Ala Glu Asp Ala			
390	395	400	
agg ggg acg ctg cct ggc cgc gtt cct gct gac caa agt cct gcc gga		1303	
Arg Gly Thr Leu Pro Gly Arg Val Pro Ala Asp Gln Ser Pro Ala Gly			
405	410	415	420
tct ggc gcc tac gag gac gtg gct ggt gga gct cag acc ggt ggg cta		1351	
Ser Gly Ala Tyr Glu Asp Val Ala Gly Gly Ala Gln Thr Gly Gly Leu			
425	430	435	

ggt ttc aac ctg cgc att ggg agg ccg aag ggt ccc cgg gac ccg cct	1399
Gly Phe Asn Leu Arg Ile Gly Arg Pro Lys Gly Pro Arg Asp Pro Pro	
440	445
450	
gct gag tgg acc cgg gtg taagtctaac gccagttcct gcctgttgcc	1447
Ala Glu Trp Thr Arg Val	
455	
tcttgtagc tcggactgct gatgccccgg tgctgctgag cgccgtgccc agaatggaaa	1507
cagtgggcct ggatcaaagt taaagttct caggggtggga aatgtggggg ctttgc当地 1567	
tgactgttagc attcaaggct tgaggctgga ggaggttagct agggtatagt ggctggtag	1627
gctgcacaga gcagattcaa gaaagaagat caggaagggg catgaccct gagttatgaa	1687
ggggagaagg gacagatgag cttccggaga ctgctctcct caccacacag cactagtcca	1747
tcctcagcac ctgagcctcc ctcacttgga cactcagggg accacacaga gaagtggatg	1807
gacacttcgc catccaggca gaactaagcc aggcataacc acagccaagc agattaaccc	1867
cagggcagacc gataaaaaga cctccagata ggcagacaga cagatggacc accaacctgg	1927
acagacagcc aaagcttcag agatacagtc cacaggtgga caaagggatc cccagccaga	1987
gagagagaga ccagccaaca gcttgataga ccagtgcagc cagagagacc accaaacaca	2047
ccccccaaaa gacagacatc tctgctagct ggacagccag gtggaccccc taagttagtc	2107
agattactag acagatataa acagatcccc tgctgaacag atatacagag ttctcagacc	2167
ccactccctc aggtgggctg gctggctgac agaccttctg gccagacaga ctcctaacc	2227
accagatgga ctgccagaca ggcagacatc agtccacatg gaatcctgac atcccagcca	2287
gccggccaga ctctcatctt gatgtcttga tggatggacc ccagctagtc agacatgatc	2347
ctccagattg acagacaagt cccccaaatg agtacacatc tccagctatt cagacagatg	2407
gagccccagc aaatcaggac ctatctaggc agaccccagc cagaccccg ccagacagac	2467
tcccaaccag actgaccctc tgctgttac acagcctgcc gagtagctgg gactacaggt	2527
ctaattttt tttttttaa gaaatgagtt tttccatgt tgcccaact ggtcttgaac	2587
tcccaaccctc aagcaatcct cctgcctcag cctcccaaag tgctgagatt acaggtgtga	2647
gccaccaggc tcagccccct aagatttcaa acactttaaa tggccatgg tagggttcct	2707
gctaggataa aacatthaagt ggctgttaaa agaaataaaa ggaggacacg tctctgtgca	2767
aaaaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa	2810

<212> PRT
 <213> Homo sapiens

<400> 36
 Met Ser Arg Ser Leu Asp Ser Ala Arg Ser Phe Leu Glu Arg Leu Glu
 1 5 10 15
 Ala Arg Gly Gly Arg Glu Gly Ala Val Leu Ala Gly Glu Phe Ser Asp
 20 25 30
 Ile Gln Ala Cys Ser Ala Ala Trp Lys Ala Asp Gly Val Cys Ser Thr
 35 40 45
 Val Ala Gly Ser Arg Pro Glu Asn Val Arg Lys Asn Arg Tyr Lys Asp
 50 55 60
 Val Leu Pro Tyr Asp Gln Thr Arg Val Ile Leu Ser Leu Leu Gln Glu
 65 70 75 80
 Glu Gly His Ser Asp Tyr Ile Asn Gly Asn Phe Ile Arg Gly Val Asp
 85 90 95
 Gly Ser Leu Ala Tyr Ile Ala Thr Gln Gly Pro Leu Pro His Thr Leu
 100 105 110
 Leu Asp Phe Trp Arg Leu Val Trp Glu Phe Gly Val Lys Val Ile Leu
 115 120 125
 Met Ala Cys Arg Glu Ile Glu Asn Gly Arg Lys Arg Cys Glu Arg Tyr
 130 135 140
 Trp Ala Gln Glu Gln Glu Pro Leu Gln Thr Gly Leu Phe Cys Ile Thr
 145 150 155 160
 Leu Ile Lys Glu Lys Trp Leu Asn Glu Asp Ile Met Leu Arg Thr Leu
 165 170 175
 Lys Val Thr Phe Gln Lys Glu Ser Arg Ser Val Tyr Gln Leu Gln Tyr
 180 185 190
 Met Ser Trp Pro Asp Arg Gly Val Pro Ser Ser Pro Asp His Met Leu
 195 200 205
 Ala Met Val Glu Glu Ala Arg Arg Leu Gln Gly Ser Gly Pro Glu Pro
 210 215 220
 Leu Cys Val His Cys Ser Ala Gly Cys Gly Arg Thr Gly Val Leu Cys
 225 230 235 240
 Thr Val Asp Tyr Val Arg Gln Leu Leu Leu Thr Gln Met Ile Pro Pro
 245 250 255
 Asp Phe Ser Leu Phe Asp Val Val Leu Lys Met Arg Lys Gln Arg Pro
 260 265 270
 Ala Ala Val Gln Thr Glu Glu Gln Tyr Arg Phe Leu Tyr His Thr Val
 275 280 285

Ala Gln Met Phe Cys Ser Thr Leu Gln Asn Ala Ser Pro His Tyr Gln
 290 295 300
 Asn Ile Lys Glu Asn Cys Ala Pro Leu Tyr Asp Asp Ala Leu Phe Leu
 305 310 315 320
 Arg Thr Pro Gln Ala Leu Leu Ala Ile Pro Arg Pro Pro Gly Gly Val
 325 330 335
 Leu Arg Ser Ile Ser Val Pro Gly Ser Pro Gly His Ala Met Ala Asp
 340 345 350
 Thr Tyr Ala Glu Glu Gln Lys Arg Gly Ala Pro Ala Gly Ala Gly Ser
 355 360 365
 Gly Thr Gln Thr Gly Thr Gly Ala Arg Ser Ala Glu Glu Ala
 370 375 380
 Pro Leu Tyr Ser Lys Val Thr Pro Arg Ala Gln Arg Pro Gly Ala His
 385 390 395 400
 Ala Glu Asp Ala Arg Gly Thr Leu Pro Gly Arg Val Pro Ala Asp Gln
 405 410 415
 Ser Pro Ala Gly Ser Gly Ala Tyr Glu Asp Val Ala Gly Gly Ala Gln
 420 425 430
 Thr Gly Gly Leu Gly Phe Asn Leu Arg Ile Gly Arg Pro Lys Gly Pro
 435 440 445
 Arg Asp Pro Pro Ala Glu Trp Thr Arg Val
 450 455

<210> 37
 <211> 503
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Mammalian SIRP4
 amino acid sequence

<400> 37
 Met Glu Pro Ala Gly Pro Ala Pro Gly Arg Leu Gly Pro Leu Leu Cys
 1 5 10 15

Leu Leu Leu Ala Ala Ser Cys Ala Trp Ser Gly Val Ala Gly Glu Glu
 20 25 30

Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Ser Val Ala Ala Gly
 35 40 45

Glu Ser Ala Ile Leu His Cys Thr Val Thr Ser Leu Ile Pro Val Gly
 50 55 60

Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Ala Arg Glu Leu Ile Tyr
 65 70 75 80
 Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Glu Ser
 85 90 95
 Thr Lys Arg Glu Asn Met Asp Phe Ser Ile Ser Ile Ser Asn Ile Thr
 100 105 110
 Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
 115 120 125
 Pro Asp Thr Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val Arg
 130 135 140
 Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala Arg Ala Thr
 145 150 155 160
 Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser Pro
 165 170 175
 Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser Asp
 180 185 190
 Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser Tyr Ser Ile
 195 200 205
 His Ser Thr Ala Lys Val Val Leu Thr Arg Glu Asp Val His Ser Gln
 210 215 220
 Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu Arg
 225 230 235 240
 Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro Thr Leu Glu
 245 250 255
 Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn Val Thr Cys
 260 265 270
 Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr Trp Leu Glu
 275 280 285
 Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val Thr Glu Asn
 290 295 300
 Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Val Ser
 305 310 315 320
 Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu His Asp Gly
 325 330 335
 Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser Ala His Pro
 340 345 350
 Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly Ser Asn Glu
 355 360 365

Arg Asn Ile Tyr Ile Val Val Gly Val Val Cys Thr Leu Leu Val Ala
 370 375 380
 Leu Leu Met Ala Ala Leu Tyr Leu Val Arg Ile Arg Gln Lys Lys Ala
 385 390 395 400
 Gln Gly Ser Thr Ser Ser Thr Arg Leu His Glu Pro Glu Lys Asn Ala
 405 410 415
 Arg Glu Ile Thr Gln Asp Thr Asn Asp Ile Thr Tyr Ala Asp Leu Asn
 420 425 430
 Leu Pro Lys Gly Lys Lys Pro Ala Pro Gln Ala Ala Glu Pro Asn Asn
 435 440 445
 His Thr Glu Tyr Ala Ser Ile Gln Thr Ser Pro Gln Pro Ala Ser Glu
 450 455 460
 Asp Thr Leu Thr Tyr Ala Asp Leu Asp Met Val His Leu Asn Arg Thr
 465 470 475 480
 Pro Lys Gln Pro Ala Pro Lys Pro Glu Pro Ser Phe Ser Glu Tyr Ala
 485 490 495
 Ser Val Gln Val Pro Arg Lys
 500

<210> 38
 <211> 398
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Mammalian SIRP1
 amino acid sequence

<400> 38
 Met Pro Val Pro Ala Ser Trp Pro His Leu Pro Ser Pro Phe Leu Leu
 1 5 10 15
 Met Thr Leu Leu Leu Gly Arg Leu Thr Gly Val Ala Gly Glu Asp Glu
 20 25 30
 Leu Gln Val Ile Gln Pro Glu Lys Ser Val Ser Val Ala Ala Gly Glu
 35 40 45
 Ser Ala Thr Leu Arg Cys Ala Met Thr Ser Leu Ile Pro Val Gly Pro
 50 55 60
 Ile Met Trp Phe Arg Gly Ala Gly Ala Gly Arg Glu Leu Ile Tyr Asn
 65 70 75 80
 Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Glu Leu Thr
 85 90 95
 Lys Arg Asn Asn Leu Asn Phe Ser Ile Ser Ile Ser Asn Ile Thr Pro
 100 105 110

Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser Pro
 115 120 125
 Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val Arg
 130 135 140
 Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Val Arg Ala Thr
 145 150 155 160
 Pro Glu His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser Pro
 165 170 175
 Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser Asp
 180 185 190
 Phe Gln Thr Asn Val Asp Pro Ala Gly Asp Ser Val Ser Tyr Ser Ile
 195 200 205
 His Ser Thr Ala Arg Val Val Leu Thr Arg Gly Asp Val His Ser Gln
 210 215 220
 Val Ile Cys Glu Met Ala His Ile Thr Leu Gln Gly Asp Pro Leu Arg
 225 230 235 240
 Gly Thr Ala Asn Leu Ser Glu Ala Ile Arg Val Pro Pro Thr Leu Glu
 245 250 255
 Val Thr Gln Gln Pro Met Arg Ala Glu Asn Gln Ala Asn Val Thr Cys
 260 265 270
 Gln Val Ser Asn Phe Tyr Pro Arg Gly Leu Gln Leu Thr Trp Leu Glu
 275 280 285
 Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Leu Ile Glu Asn
 290 295 300
 Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Thr Cys
 305 310 315 320
 Ala His Arg Asp Asp Val Val Leu Thr Cys Gln Val Glu His Asp Gly
 325 330 335
 Gln Gln Ala Val Ser Lys Ser Tyr Ala Leu Glu Ile Ser Ala His Gln
 340 345 350
 Lys Glu His Gly Ser Asp Ile Thr His Glu Pro Ala Leu Ala Pro Thr
 355 360 365
 Ala Pro Leu Leu Val Ala Leu Leu Gly Pro Lys Leu Leu Leu Val
 370 375 380
 Val Gly Val Ser Ala Ile Tyr Ile Cys Trp Lys Gln Lys Ala
 385 390 395

<210> 39
 <211> 495
 <212> PRT
 <213> Mus musculus

<400> 39
 Pro Arg Pro Arg Lys Tyr His Ser Ser Glu Arg Gly Ser Arg Gly Ser
 1 5 10 15
 Tyr His Glu His Tyr Gln Ser Arg Lys His Lys Arg Arg Arg Ser Arg
 20 25 30
 Ser Trp Ser Ser Ser Asp Arg Thr Arg Arg Arg Ala Arg Glu Asp
 35 40 45
 Ser Tyr His Val Arg Ser Arg Ser Ser Tyr Asp Asp His Ser Ser Asp
 50 55 60
 Arg Arg Leu Tyr Asp Arg Arg Tyr Cys Gly Ser Tyr Arg Arg Asn Asp
 65 70 75 80
 Tyr Ser Arg Asp Arg Gly Glu Ala Tyr Tyr Asp Thr Asp Phe Arg Gln
 85 90 95
 Ser Tyr Glu Tyr His Arg Glu Asn Ser Ser Tyr Arg Ser Gln Arg Ser
 100 105 110
 Ser Arg Arg Lys His Arg Arg Arg Arg Arg Ser Arg Thr Phe Ser
 115 120 125
 Arg Ser Ser Ser His Ser Ser Arg Arg Ala Lys Ser Val Glu Asp Asp
 130 135 140
 Ala Glu Gly His Leu Ile Tyr His Val Gly Asp Trp Leu Gln Glu Arg
 145 150 155 160
 Tyr Glu Ile Val Ser Thr Leu Gly Glu Gly Thr Ser Gly Arg Val Val
 165 170 175
 Gln Cys Ile Asp Arg Arg Val Gly Thr Arg Arg Val Leu Val Ile Ile
 180 185 190
 Lys Asn Val Glu Lys Tyr Lys Glu Ala Ala Arg Leu Glu Ile Asn Val
 195 200 205
 Leu Glu Lys Ile Asn Glu Lys Asp Pro Lys Asn Lys Asn Leu Cys Val
 210 215 220
 Gln Met Phe Asp Trp Phe Asp Tyr His Gly His Met Cys Ile Ser Phe
 225 230 235 240
 Glu Leu Leu Gly Leu Ser Thr Phe Asp Phe Leu Lys Asp Asn Asn Tyr
 245 250 255
 Leu Pro Tyr Pro Ile His Gln Val Arg His Met Ala Phe Gln Leu Cys
 260 265 270

Gln Ala Val Lys Phe Leu His Asp Asn Lys Leu Thr His Thr Asp Leu
 275 280 285

 Lys Pro Glu Asn Ile Leu Phe Val Asn Ser Asp Tyr Glu Leu Thr Asn
 290 295 300

 Pro Leu Glu Lys Arg Asp Glu Arg Thr Ser Val Lys Ser Thr Ala Val
 305 310 315 320

 Arg Val Asp Phe Gly Ser Ala Thr Tyr Phe Asp His His Ser Thr
 325 330 335

 Leu Ile Ser Thr Arg His Tyr Arg Ala Pro Glu Val Ile Leu Glu Leu
 340 345 350

 Gly Trp Ser Gln Pro Cys Asp Val Trp Ser Ile Gly Cys Ile Phe Ile
 355 360 365

 Glu Tyr Val Leu Gly Phe Leu Val Gln Pro Thr His Asn Ser Arg Glu
 370 375 380

 His Leu Ala Met Glu Arg Ile Leu Gly Pro Val Pro Ser Arg Met Ile
 385 390 395 400

 Arg Lys Thr Arg Lys Gln Lys Tyr Phe Tyr Arg Gly Arg Leu Asp Trp
 405 410 415

 Asp Glu Asn Thr Ser Ala Gly Arg Tyr Val Arg Glu Asn Cys Lys Pro
 420 425 430

 Leu Arg Arg Tyr Leu Thr Ser Glu Ala Glu Asp His His Gln Leu Phe
 435 440 445

 Asp Leu Ile Glu Asn Met Leu Glu Tyr Glu Pro Ala Lys Arg Leu Thr
 450 455 460

 Leu Gly Glu Ala Leu Gln His Pro Phe Phe Ala Cys Leu Arg Thr Glu
 465 470 475 480

 Pro Pro Asn Thr Lys Leu Trp Asp Ser Ser Arg Asp Ile Ser Arg
 485 490 495

<210> 40
 <211> 484
 <212> PRT
 <213> *Mus musculus*

<400> 40
 His Arg Cys Ser Lys Tyr Arg Ser Pro Glu Pro Asp Pro Tyr Leu Thr
 1 5 10 15

 Tyr Arg Trp Lys Glu Arg Arg Ser Asp Ser Arg Glu His Glu Gly Arg
 20 25 30

 Leu Arg Tyr Pro Ser Arg Lys Glu Pro Pro Pro Arg Ala Ser Ser Arg
 35 40 45

Glu Asp Ala Pro Tyr Arg Thr Arg Lys His Ala His His Cys His Lys
 50 55 60

Ile Arg Thr Arg Ser Cys Ser Ser Ala Ser Ser Arg Ser Gln Gln Ser
 65 70 75 80

Ser Lys Arg Ser Ser Arg Gly Glu Ser Arg Glu Arg Ala Pro Tyr Arg
 85 90 95

Thr Arg Lys His Ala His His Cys His Lys Arg Arg Thr Arg Ser Cys
 100 105 110

Ser Ser Ala Ser Ser Arg Ser Gln Gln Ser Ser Lys Arg Ser Ser Arg
 115 120 125

Ser Val Glu Asp Asp Lys Glu Gly His Leu Val Cys Arg Ile Gly Ser
 130 135 140

Trp Leu Gln Glu Arg Tyr Glu Ile Val Gly Asn Leu Gly Glu Gly Thr
 145 150 155 160

Phe Gly Lys Val Val Glu Cys Leu Asp His Ala Arg Gly Lys Ser Gln
 165 170 175

Val Ala Leu Lys Ile Ile Arg Asn Val Gly His Tyr Arg Glu Ala Ala
 180 185 190

Arg Leu Glu Ile Asn Val Leu Lys Lys Ile Lys Glu Lys Asp Lys Glu
 195 200 205

Asn Lys Phe Leu Cys Val Leu Met Ser Asp Trp Asn Phe His Arg Gly
 210 215 220

Met Ile Cys Ala Val Glu Leu Leu Gly Lys Asn Thr Phe Glu Phe Leu
 225 230 235 240

Lys Glu Asn Asn Phe Gln Pro Tyr Pro Leu Pro His Val Arg His Met
 245 250 255

Ala Tyr Gln Leu Cys His Ala Leu Arg Phe Leu His Glu Asn Gln Leu
 260 265 270

Thr His Thr Asp Leu Lys Pro Glu Asn Ile Leu Phe Val Asn Ser Asp
 275 280 285

Glu Phe Glu Thr Leu Pro Lys Glu His Lys Ser Cys Glu Thr Lys Ser
 290 295 300

Val Lys Asp Thr Ser Ile Arg Asp Ala Gly Ser Ala Thr Tyr Asp Phe
 305 310 315 320

Glu His His Ser Thr Thr Val Ile Ala Thr Arg His Tyr Arg Pro Pro
 325 330 335

Glu Val Ile Leu Glu Leu Gly Trp Ala Gln Pro Cys Asp Val Trp Ser
 340 345 350

Ile Gly Cys Ile Leu Phe Glu Tyr Tyr Arg Gly Phe Thr Leu Phe Gln
 355 360 365
 Thr His Asp Ser Lys Glu His Leu Ala Met Met Glu Lys Ile Leu Gly
 370 375 380
 Pro Ile Pro Ser His Met Ile His Arg Thr Arg Lys Gln Lys Tyr Phe
 385 390 395 400
 Tyr Lys Gly Gly Leu Val Trp Asp Glu Asn Ser Ser Asp Gly Arg Tyr
 405 410 415
 Val Lys Glu Asn Cys Lys Pro Leu Lys Ser Tyr Met Leu Gln Asp Ser
 420 425 430
 Leu Glu His Val Gln Leu Phe Asp Leu Met Arg Arg Met Leu Glu Phe
 435 440 445
 Asp Pro Ala Gln Arg Ile Thr Leu Ala Glu Ala Leu Leu His Pro Phe
 450 455 460
 Phe Ala Gly Leu Thr Pro Glu Glu Arg Ser Phe His Ser Ser Ser Arg
 465 470 475 480
 Asn Pro Ser Arg

<210> 41
 <211> 481
 <212> PRT
 <213> Mus musculus

<400> 41
 Met Arg His Ser Lys Arg Thr His Cys Pro Asp Trp Asp Ser Arg Glu
 1 5 10 15
 Ser Trp Gly His Glu Ser Tyr Ser Gly Ser His Lys Arg Lys Arg Arg
 20 25 30
 Ser His Ser Ser Thr Gln Glu Asn Arg His Cys Lys Pro His His Gln
 35 40 45
 Phe Lys Asp Ser Asp Cys His Tyr Leu Glu Ala Arg Cys Leu Asn Glu
 50 55 60
 Arg Asp Tyr Arg Asp Arg Arg Tyr Ile Asp Glu Tyr Arg Asn Asp Tyr
 65 70 75 80
 Cys Glu Gly Tyr Val Pro Arg His Tyr His Arg Asp Val Glu Ser Thr
 85 90 95
 Tyr Arg Ile His Cys Ser Lys Ser Ser Val Arg Ser Arg Arg Ser Ser
 100 105 110
 Pro Lys Arg Lys Arg Asn Arg Pro Cys Ala Ser His Gln Ser His Ser
 115 120 125

Lys Ser His Arg Arg Lys Arg Ser Arg Ser Ile Glu Asp Asp Glu Glu
 130 135 140

Gly His Leu Ile Cys Gln Ser Gly Asp Val Leu Arg Ala Arg Tyr Glu
 145 150 155 160

Ile Val Asp Thr Leu Gly Glu Gly Ala Phe Gly Lys Val Val Glu Cys
 165 170 175

Ile Asp His Gly Met Asp Gly Leu His Val Ala Val Lys Ile Val Lys
 180 185 190

Asn Val Gly Gly Tyr Arg Glu Ala Ala Arg Ser Glu Ile Gln Val Leu
 195 200 205

Glu His Leu Asn Ser Thr Asp Pro Asn Ser Val Phe Arg Cys Val Gln
 210 215 220

Met Leu Glu Trp Phe Asp His His Gly His Val Cys Ile Val Phe Glu
 225 230 235 240

Leu Leu Gly Leu Ser Thr Tyr Asp Phe Ile Lys Glu Asn Ser Phe Leu
 245 250 255

Pro Phe Gln Ile Asp His Ile Arg Gln Met Ala Tyr Gln Ile Cys Gln
 260 265 270

Ser Ile Asn Phe Leu His His Asn Lys Leu Thr His Thr Asp Leu Lys
 275 280 285

Pro Glu Asn Ile Leu Phe Val Lys Ser Asp Tyr Val Val Lys Asn Pro
 290 295 300

Ser Met Lys Arg Asp Glu Arg Thr Ile Leu Lys Pro Thr Asp Ile Lys
 305 310 315 320

Val Val Asp Phe Gly Ser Ala Thr Tyr Asp Asp Glu His His Ser Thr
 325 330 335

Leu Val Ser Thr Arg His Tyr Arg Ala Pro Glu Val Ile Leu Ala Leu
 340 345 350

Gly Trp Ser Gln Pro Cys Asp Val Trp Ser Ile Gly Cys Ile Leu Ile
 355 360 365

Glu Tyr Tyr Leu Gly Phe Thr Val Phe Gln Thr His Asp Ser Lys Glu
 370 375 380

His Leu Ala Met Met Glu Arg Ile Leu Gly Pro Ile Pro Ala His Met
 385 390 395 400

Ile Gln Lys Thr Arg Lys Arg Lys Tyr Phe His His Asn Gln Leu Asp
 405 410 415

Trp Asp Glu His Ser Ser Ala Gly Arg Tyr Val Arg Arg Cys Lys
 420 425 430

40

Pro Leu Lys Glu Phe Met Leu Cys His Asp Glu Glu His Glu Lys Leu
435 440 445

Phe Asp Leu Val Arg Arg Met Leu Glu Tyr Asp Pro Ala Arg Arg Ile
450 455 460

Thr Leu Asp Glu Ala Leu Gln His Pro Phe Phe Asp Leu Leu Lys Arg
465 470 475 480

Lys